

Contemporary Biosocial Criminology: A Systematic Review of the Literature, 2000–2012

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With few exceptions, sociological thinking dominates the field of criminology (Walsh & Ellis, 2004). Peering through the walls of the discipline's framework, one can sometimes see traces of psychology, political science, and economics staring blankly back, yet the foundation of the field is clearly built on sociological theorizing. The vague specter of other disciplines (psychology, economics, etc.) is enough to provide the criminological student with the impression that the field is inherently interdisciplinary. But students are often surprised to hear that biological research is not interwoven more into the fabric of criminological discourse.

The more that one becomes acquainted with the state of the field the more it becomes apparent that criminology is bereft of many important advances uncovered in the hard sciences (Wright *et al.*, 2008). Specifically, the hegemony of sociological viewpoints has steered the field away from developments in biology, genetics, and evolutionary psychology (Udry, 1995). Despite criminology's insulation, a strand of biologically oriented scholarship has recently gained momentum. Referred to broadly as "biosocial criminology," this nascent body of literature has revealed a genetic link to criminal behavior (Raine, 1993; Rowe, 2001), that our evolutionary past is important to understand if we wish to know the origins of aggression and risky behavior (Ellis *et al.*, 2011), and that many of the "classic" studies in the criminological literature may have been misspecified due to the omission of biological/genetic variables (Wright & Beaver, 2005).

Bringing these points to bear is the primary concern of the emerging paradigm of biosocial criminology. This body of knowledge differs from the standard sociological viewpoint in many ways. For example, genetic influences on behavior are expected by biosocial criminology and their interaction with environmental factors

has become one of the hallmark findings of the 20th and 21st centuries. Moreover, biosocial criminology proffers many new questions about the origins of criminality and it offers insight into some of the least understood associations known to criminologists (Udry, 1995). Though biosocial criminology is often linked with "Lombrosian" criminology, contemporary scholars have, in just a few years, amassed an important base of information about the biological and genetic influences on criminality and criminal behavior. Meta-analyses and literature reviews concerning certain aspects of the biosocial paradigm have emerged in recent years (e.g., Burt, 2009; Ferguson, 2010; Moffitt, 2005; Moffitt *et al.*, 2011; Rhee & Waldman, 2002) but a review tailored to biosocial research appearing in criminology journals has not yet been presented. The current study will fill this gap in the literature by offering a systematic review of the contemporary biosocial criminology literature. Before doing so, however, it is important to gain a conceptual understanding of biosocial criminology and its research domains.

What is Biosocial Criminology?

Biosocial criminology is best understood as a general paradigm of research that analyzes biological, environmental, and sociological factors related to criminal behavior. Biosocial criminology highlights the importance of genetic effects, biological factors such as hormone levels, neurological events, societal influences, and even family influences in the etiology of antisocial behavior. In this way, *biosocial criminology* is a blanket concept that includes at least five major domains: evolutionary criminology, biological criminology, behavior genetics, molecular genetics, and neurocriminology. Each of the five domains will be described, and the literature bearing on these domains will be discussed below. It is important to note that none of the domains are mutually exclusive. To be sure, each domain must be blended with the others to attain a full picture of the origins of antisocial behavior, but separating them in this manner will facilitate an understanding of their interrelatedness and offers an avenue by which we can summarize the extant literature.

Evolutionary criminology

As outlined by Quinsey (2002), evolutionary explanations of criminal behavior seek the "ultimate" causes in contrast to the standard focus on "proximal" causes. Ultimate causes of behavior are those that have been shaped by evolutionary forces over the deep time of evolution while proximal causes are the specific developmental, genetic, and environmental variables that criminologists typically seek out. For these reasons, evolutionary criminology may be able to offer insight into some of the most elusive questions faced by criminologists such as "Why are males overinvolved in violence?" and "Why does risky behavior peak during adolescence?" In order to answer these questions, evolutionary criminologists apply the principles of evolution by natural selection (Darwin, 1859) to human behavior (Tooby & Cosmides, 2005).

Other prominent scholars in the area of evolutionary psychology have provided thorough and thoughtful overviews of the field (Buss, 2009). We direct the reader to these additional volumes; however, a brief conceptualization of basic ideas is offered here. Evolutionary psychology – and by extension evolutionary criminology – views humans as being the product of millions of years of selection pressures (just like every other organism on the planet). Just as selection forces “designed” complex devices like the eye and the heart, these same forces (either directly or indirectly) would have also designed the mind along with everything that the mind does (Pinker, 2002). Evolution favored aspects of the mind that were adept at solving ancestral problems, most notably survival and reproduction.

In this regard, evolutionary psychology offers an explanation for the etiology of a wide range of human phenotypes, including some of the most heinous acts committed in the natural world. Daly & Wilson (1988), for instance, argued that evolutionary criminology offered an explanation and unique understanding of most types of homicides (e.g., infanticide, patricide, etc.). The key to understanding these abhorrent acts is to know something about the motivations of human behavior by linking them with our ancient ancestor’s environment and the problems faced there. In short, evolutionary criminologists seek to understand contemporary humans’ behavior by looking for the origins of that behavior in our remote environmental past, the African Savannah.

Another benefit of evolutionary criminology is that it offers an explanation of why certain characteristics appear to be universal across virtually all human cultures. Research has revealed that, while cultures differ in their tolerance of violence and aggression, all human cultures recognize certain acts, like intra-group homicide, to be antisocial (Brown 1991; Pinker, 2011). Another human universal is the sex gap in violence (as well as aggression), a finding that is so consistent that it may not be entirely inappropriate to canonize it as a “law” of criminology. The sex gap has proven invariant across cultures and across time (Campbell, 2009), suggesting evolutionary criminology may have insight on the issue. The sex gap, for instance, may reflect the unique evolutionary pressures placed on both males and females, a claim bolstered all the more by the uniformity of human behavior across cultural boundaries. In short, the sex bearing the largest parental investment (females)¹ should be expected to display fewer “risky” behaviors as a way to maximize their reproductive potential – which is precisely what the evidence bears out. In summary, evolutionary criminology seeks an understanding of the “ultimate” causes of criminal behavior by referring to universal patterns of human behavior that date back to our ancestors’ time on the African Savannah.

Biological criminology

One stream of biosocial criminological research focuses on the physiological factors, not just genetic factors that may be related to antisocial behavior. Though many of the genetic effects identified by behavioral and molecular genetics research is likely

to work through physiological factors, it remains important to understand these mediating mechanisms. Three primary types of biological criminology research can be identified in the extant literature. First is research into hormonal linkages to anti-social behavior. Testosterone is one hormone that has received much attention and it is hypothesized to explain a portion of the sex gap in violent behavior. In general, research has shown testosterone levels to be correlated with aggressive and dominant behavior, but the temporal/causal ordering remains unclear. Testosterone levels can vary throughout the day, and baseline averages in testosterone levels fluctuate across the life-course. As a result, it is difficult to disentangle the exact mechanisms underlying the testosterone-aggression correlation (Archer, 2006; Mazur, 2009).

A second line of biological research in criminology has focused on resting heart-rate levels (Armstrong & Boutwell, 2012; Ortiz & Raine, 2004; Raine *et al.*, 1997). Resting heart-rate levels are thought to influence autonomic arousal levels that, in turn, influence sensation-seeking behaviors. Ortiz & Raine (2004) performed a meta-analysis on the available literature and reported a robust correlation between resting heart-rate and antisocial behavior. More directly, these authors revealed a consistent correlation between resting heart-rate and sensation-seeking behaviors, suggesting it is an important correlate of antisocial, aggressive, and perhaps even criminal involvement.

Finally, the third type of biological criminology research analyzes the role of pubertal onset/development in the etiology of antisocial behavior in adolescence (e.g., Barnes & Beaver, 2010; Haynie, 2003). These studies have consistently linked biological development with behavior, indicating the importance of such variables in criminological models and theories (Moffitt, 1993). Most studies have reported that early onset of puberty is associated with a relative increase in the risk of antisocial behavior, drug use, and general problem behaviors (e.g., Haynie, 2003).

Behavior genetics

Behavior genetic research offers scientists a way to analyze both genetic and environmental influences on human behaviors and personality traits. To do so, behavioral geneticists rely on a key piece of information; different types of sibling pairs vary in the amount of genetic material that they share. Usually, the focus is on twins, wherein monozygotic twins (MZ twins, or, better known as identical twins) share 100 percent of their DNA while dizygotic twins (DZ twins, or, better known as fraternal twins) share only 50 percent of their distinguishing DNA on average. Capitalizing on this fact of nature allows behavior geneticists to estimate the relative contribution of heritability (h^2), shared environmental (c^2) effects, and nonshared environmental (e^2) effects in the etiology of behavioral outcomes. The heritability component (h^2) measures the amount of variance in a phenotype that can be attributed to genetic differences in the sample. A heritability estimate of .75, for example, would mean that three-fourths (75%) of the variance in the measure of interest is attributable to differences in genetic material between the respondents in

the sample. The environmental components (i.e., c^2 and e^2) estimate the amount of variance in the phenotype that can be attributed to environmental factors. It is important to point out the shared (c^2) environment captures environmental influences that make two siblings more alike. For this reason, the shared environment is often believed to tap into parenting influences. Nonshared environmental influences (e^2) capture environmental effects that make siblings different from one another. Nonshared environments may capture, for instance, stochastic environmental effects or events where siblings have differing subjective interpretations or perceptions of the incident (Turkheimer & Waldron, 2000). Measurement error is also captured by the nonshared environmental component.

As mentioned above, behavior geneticists often rely on sets of twin pairs to estimate the relative contribution of heritability, the shared environment, and the nonshared environment in the variance of a trait. To be sure, behavior geneticists often utilize samples of twins (Plomin *et al.*, 2012), but it is possible to include other types of respondent pairs as long as the researcher indexes the individuals' level of genetic relatedness. For instance, some scholars have analyzed samples of adoptees to determine the relative contribution of genetic and environmental influences to behavior (Raine, 1993). One classic study revealed a correlation between adoptees' criminal records and their biological parents' criminal record (Mednick *et al.*, 1984). Specifically, Mednick and colleagues (1984) found that adoptees whose biological parents had a criminal record were more likely to have a criminal record as compared to adoptees whose parents did not have a criminal record.

In general, behavior genetic studies have emerged as one of the most popular methods among biosocial criminologists and, as a result, much is now known concerning the link between genetics and criminality. Recent meta-analyses have summarized the role of genetic and environmental influences in the etiology of aggression, delinquency, criminality, and other related phenotypes (Burt, 2009; Ferguson, 2010; Rhee & Waldman, 2002). These meta-analyses suggested that antisocial behavior is around 50 percent heritable, with the remaining variance being attributable primarily to nonshared environmental factors.

Molecular genetics

Around the turn of the 21st century, genomic sciences took a huge leap forward when the human genome was successfully mapped. The mapping of the human genome was a harbinger for significant scientific advances on the horizon. Criminologists who are interested in unpacking the genetic influences on antisocial behavior have begun to rely on molecular genetics research methods to inform their studies (Beaver, 2009; Carey, 2003). To be brief, molecular genetics research involves identifying specific genes that may be associated with antisocial behavior. In order to comprehend how this might be possible, it is important to understand exactly what a gene is. Inside the nucleus of every cell in the human body (with the exception of red blood cells) is a set of 23 chromosomes (two each, 46 total). Wound around

each chromosome is deoxyribonucleic acid, otherwise known as DNA. (Note that this is an oversimplification. See Snustad & Simmons (2012) for more detail.) DNA has a helical structure (think of a ladder that has been twisted in opposite directions on each end) and is made up of a sugar phosphate backbone (the sides of the ladder) and four nucleic acid base pairs (the rungs of the ladder). The base pairs are referred to as A, T, C, and G – the genetic alphabet – and can be written like so:

AATCGTTTCGTGACGTAAGATTACGCCTCCT

The string of letters above might represent a portion of DNA. Imagine that the underlined set of contiguous letters worked together to perform a function in the human body. If this were the case, we could call this string of letters (GTGACGTAAGAT) a gene. Scientists estimate that humans carry around 23,000 genes. Interestingly, however, most humans carry the exact same genetic sequence for the large majority of genes. Indeed, only a fraction of the human genome is believed to differ from person to person – referred to as “distinguishing DNA” or “genetic polymorphisms.” In large part, it is this portion of the human genome that molecular geneticists focus on when they are interested in explaining differences from one person to the next.

Recognizing these points, a body of criminological evidence has begun to accumulate showing a link between certain genetic polymorphisms and antisocial behaviors. Genetic polymorphisms have been linked to well-known predictors of antisocial behaviors such as ADHD (Faraone *et al.*, 2001) and gang membership (Beaver, DeLisi, Vaughn, & Barnes, 2010). Perhaps more important, molecular genetics research has demonstrated the importance of understanding the synergistic relationship between environmental stimuli and genetic influences on behavior. Referred to as gene-by-environment interaction (G×E), research has shown that certain genetic effects are more likely to manifest when combined with environmental risk factors like growing up in an adverse rearing environment (Caspi *et al.*, 2002). In other words, changes in the environment can alter the effects of genetic factors.

Neurocriminology

Criminologists are beginning to recognize the importance of neurological mechanisms in the etiology of human behavior (Moffitt *et al.*, 2011). Of particular importance is that many of the influences discussed in this review (i.e., genes, hormones) must impact behavior *via* their impact on the brain (Raine, 2008). The brain is the epicenter for all human behavior and emotions. Neuroscience research has clearly demonstrated that certain regions of the brain appear to be critically important for understanding the etiology of antisocial behavior (Raine *et al.*, 2003; Yang *et al.*, 2005). As Raine (2008) explained, it is likely that most of the evolutionary, genetic, and biological risk factors that have been linked to antisocial

behavior are mediated by the brain such that a gene that impacts antisocial behavior must manifest its impact on either the structure or the functioning of the brain.

Though neurocriminology provides important insight into the etiology of human behavior, most of the relevant literature appears in journals outside the boundaries of the criminological discipline and, therefore, were not captured by our literature search (see below). It is worth noting, however, an important line of criminological research has examined the link between direct measures of neurological functioning and criminality (Gilligan & Lennings, 2011; Mednick *et al.*, 1981). Many scholars have analyzed the role of indicators of neuropsychological deficits (Piquero, 2001; Moffitt, 1990) such as levels of self-control (Muraven *et al.*, 2006; Pratt & Cullen, 2000), birth complications (Beaver, Vaughn, DeLisi, & Higgins, 2010c), history of traumatic brain injury (Farrer *et al.*, 2012), and serious mental illness (Swartz & Lurigio, 2007) in the prediction of antisocial behaviors. We omit these studies from the current review for one primary reason: the degree to which criminological measures of neuropsychological deficits overlap with neurocriminological concepts is unclear at this point (but see Martens (2002) and Walsh & Bolen (2012) for a cogent review and conceptual discussion). Including neurocriminology in the present review would have forced many arbitrary decisions concerning which studies to include and which studies to exclude. Rather than risk potential bias in the review findings, we opted to omit this domain from the analysis presented below.

The current focus

Contemporary biosocial criminology appreciates the complex etiology of antisocial behavior and, as a result, recognizes that such behavioral outcomes are unlikely to be the result of one influential factor. Instead, it is likely that a combination of genetic effects, biological influences, neurological events, and even environmental triggers are implicated in the origins of antisocial behavior. Further, evolutionary criminology suggests that these influences are likely to be rooted in our deep evolutionary history, probably dating back to at least our early human ancestors. Though biosocial criminology has been around for decades – perhaps dating back to the 1800s with Lombroso – it has only recently begun to emerge as a viable strand of criminological thought. As such, the purpose of this paper is to review recent biosocial criminology research appearing in criminology journal outlets. As will be described below, we performed a systematic literature search for any paper bearing on the biosocial criminology paradigm that has been published in a criminology journal since the turn of the 21st century. The work retrieved by this literature search touched on four of the five biosocial criminology domains: biological criminology, evolutionary criminology, behavior genetics, and molecular genetics. Recall that neurocriminology was omitted from the analysis due to the small number of articles that have been published in criminology journals.

Literature Search Process and Inclusion Criteria

The literature search was conducted using the Web of Science (WOS) search engine on December 19, 2012. The WOS search engine was accessed and the following search criteria were entered into an "Advanced Search": "TI = (biosocial OR gene* OR evolution* OR biolog*) AND SU = Criminology & Penology." Specifically, we searched WOS for any article published in a journal included in the "Criminology & Penology" subject category that was written in English and used the term "biosocial," "gene*," "evolution*," or "biolog*" in its title. Note that several of the search terms included a wild card character (i.e., *). This allowed for the inclusion of any article that included the root term (e.g., "gene") but also included a suffix on that term. For instance, by including the wild card on the search term, gene, the search engine gathered any study that used the word "gene" as well as any study that included the word "genetic". The WOS search was restricted to papers published between January 1, 2000 and 12/1/2012. As noted above, our focus was on contemporary biosocial criminology research. We recognize that biosocial research appeared in criminology journals prior to the year 2000 and we have made reference to many of these studies in the introduction to this analysis. Note, however, that the goal of the present study was to "take stock" of recent biosocial criminology analyses. As such, we limited the search to papers published since 2000.

The WOS search netted a total of 314 articles. Because of the use of the wild cards, however, not all 314 papers were expected to meet our inclusion criteria. Specifically, each of the 314 articles was manually inspected to identify those that were appropriate for the analysis. Two primary inclusion criteria were implemented. First, it was necessary to determine which of the 314 articles presented a biosocial analysis. Due to the inclusion of the wild card (*) on the term "gene," a large number of studies were identified because they used the term "general" in the title. This was expected, but meant that we ended up with a large number of studies that were inappropriate for the analysis. For instance, a significant portion of the article pool included studies testing Agnew's (1992) general strain theory or those testing Gottfredson & Hirschi's (1990) *General Theory of Crime*. Thus, it was necessary to identify these articles and remove them from the pool of eligible papers. The second inclusion criterion was that only articles presenting a new empirical investigation were included. Although none of the 314 papers were qualitative studies (but see generally, Halsey & Deegan, 2012), a significant number were review papers, discussion pieces, or purely theoretical considerations of a biosocial concept or the integration of biosocial criminology with sociological criminology. These types of articles were removed from the analytic frame, though many have been cited in the introduction to this chapter. Implementation of the inclusion criteria trimmed the usable number of studies to a total of 41.

Before moving to the findings of the review, it is worth noting that a few papers were loosely related to the biosocial paradigm but were not included in the analysis because they did not directly test a biosocial hypothesis. For instance, several studies were gleaned that analyzed the intergenerational transmission of crime/delinquency in families (Bijleveld & Wijkman, 2009; Kim *et al.*, 2009; Novero *et al.*,

2011; Ramakers *et al.*, 2011; Smith *et al.*, 2011). These studies are acknowledged here because the intergenerational transmission of crime is an important issue and the predictions made by biosocial criminology are clear: genetic inheritance explains a portion of the intergenerational transmission of behavior. Each study reported evidence to support the notion that crime “runs in families” but it is unclear from the available information whether the cross-generation correlation in criminal status is the result of inherited genetic factors, socialization factors, or some combination of both (though see Bijleveld & Wijkman, 2009 for a consideration of these points).

Findings

Presented below is a summary of the biosocial criminology research that has been published in a criminology journal outlet since 2000. All relevant research studies are summarized according to the biosocial criminology domain to which they correspond. Recall that neurocriminology was omitted from the analysis due to the small number of articles that have been published in criminology journals.

Evolutionary criminology findings

Several evolutionary criminological studies were identified ($n = 11$), but only two offered an empirical test of evolutionary hypotheses (Michalski *et al.*, 2007; Zwirs *et al.*, 2012).² Michalski and colleagues, working from an evolutionary perspective, analyzed siblicides (the killing of one's sibling[s]) in Chicago between 1870 and 1930. Based on evolutionary theory, the authors developed two hypotheses. First, they hypothesized that siblicides where the victim was a sibling-in-law would be more likely to be perpetrated by beating as compared to siblicides where the victim was a full sibling. The second hypothesis was that siblicides where the victim was a full sibling would be more likely to result from accidental circumstances than siblicides where the victim was a sibling-in-law. The authors found evidence to support both hypotheses by showing that beatings were more prevalent when the victim was a sibling-in-law and that accidental homicide was more prevalent when the victim was a full sibling. Statistical tests indicated that only the latter (full siblings more likely to die as the result of an accident) was statistically significant.

Zwirs and colleagues (2012) analyzed the phenotypic correlation between males and females in a marital, cohabiting, or dating relationship; a phenomenon referred to as “assortative mating” by evolutionary criminologists. To be brief, evolutionary criminology suggests individuals will prefer to mate with others who are like themselves, but of the opposite sex. Zwirs *et al.* (2012) reported evidence to support this notion by showing that couples correlated positively for many measures of antisocial behavior such as property crime, violence, and arrest records. Evidence for sorting based on shared environments rather than on behavior did emerge, however. Specifically, partner similarity for violent behavior was reduced when demographic factors were controlled.

Biological criminology findings

As noted in the introduction, a body of research has explored the role of biological functioning (broadly defined) in the etiology of antisocial behavior. The analytic review uncovered several studies that can be classified as informing the biological criminology domain. Maletzky & Field (2003) reviewed the literature on hormonal treatment and sexual offending recidivism and performed an analysis on a pilot study that used hormonal treatment on sex offenders. The findings reported by these authors were promising in terms of the efficacy of hormonal treatment programs. Another study identified in the analysis had bearing on the correlation between resting heart-rate and criminality (Armstrong & Boutwell, 2012). Armstrong & Boutwell (2012) reported that college students who had a low resting heart-rate were less likely to be deterred from antisocial behavior as compared to those without a low resting heart-rate. In short, individuals with low resting heart-rate may be less deterrable from offending.

Other biological criminology studies analyzed the impact of environmental pathogens such as exposure to cigarette smoke (post-natal) and verbal IQ. Beaver and colleagues (2010c) reported a negative association between exposure to cigarette smoke and verbal IQ such that respondents exposed to cigarette smoke scored lower on the verbal IQ task. Beaver *et al.* (2010c) also reported a correlation between length of breastfeeding and verbal IQ. Respondents who were breastfeed longer performed better on the verbal IQ test. In a related analysis, Ratchford & Beaver (2009) reported that respondents who experienced birth complications and those of lower birth weight had reduced verbal IQ scores as compared to respondents who did not experience birth complications or those of higher birth weight.

Three studies integrated a biological focus into Agnew's (1992) general strain theory. First, Jackson (2012) reported that the effect of strain on delinquency may be contingent upon pubertal development such that youth who experience early puberty may be more affected by strain than youth who have not yet experienced puberty. The second study, conducted by Stogner & Gibson (2010), reported a link between physical health strains and non-violent offending frequency. Specifically, respondents who experienced greater physical strains reported a greater frequency of non-violent offending. Third, Schroeder *et al.* (2011) similarly found that respondents who reported poor physical health (or who experienced reductions in physical health) were more likely to onset in offending (or continue offending) as compared to those who did not experience poor health (or reductions in health).

Behavior genetic findings

As can be seen in Table 5.1, the total number of behavior genetic studies is greater than any other type of biosocial criminology research domain. Indeed, 19 of the 41 studies included in the analysis were behavior genetic analyses. Rather than identify studies one-by-one, a general summary of the overall findings is offered here.

Table 5.1 Summary of Biosocial Criminology Research, 2000–2012

<i>Author(s)</i>	<i>Year</i>	<i>Data</i>	<i>Analysis Type</i>	<i>Primary Finding(s)</i>
Michalski <i>et al.</i>	2007	Chicago	Evolutionary Criminology	Cause of suicide varies according to sibling relatedness. Victims who are sibling-in-law are more likely to be beaten. Victims who are full siblings are more likely to die from an accident.
Zwirs <i>et al.</i>	2012	Gen. R	Evolutionary Criminology	Romantic partners correlate for many types of antisocial behavior. For most behaviors, the correlation was unaffected by controlling for demographic factors, suggesting partners select others who display similar levels of antisocial behavior.
Armstrong & Boutwell	2012	Students	Biological Criminology	Students with low resting heart-rate were less likely to be deterred from antisocial behavior.
Beaver <i>et al.</i>	2010(c)	Add Health	Biological Criminology	Postnatal exposure to smoke and duration of breastfeeding predict verbal IQ in adolescence.
Jackson	2012	Add Health	Biological Criminology	The effect of strain on delinquency is moderated by the respondent's level of pubertal development. Those who experience early puberty are more sensitive to strains.
Maletzky & Field	2003	Oregon	Biological Criminology	Pilot study on hormonal treatment for sex offenders indicates promising outlook for reducing recidivism.
Ratchford & Beaver	2009	Add Health	Biological Criminology	Birth complications and low birth-weight predict verbal IQ in adolescence and may indirectly influence self-control and delinquency via verbal IQ.
Schroeder <i>et al.</i>	2011	WCF	Biological Criminology	Poor physical health predicts offending onset or escalations in offending patterns and is mediated by depression and anxiety.
Stogner & Gibson	2010	Add Health	Biological Criminology	Health strains increase involvement in nonviolent delinquency.

(Continued)

Table 5.1 (Continued)

Author(s)	Year	Data	Analysis Type	Primary Finding(s)
Barnes & Beaver	2012	Add Health	Behavior Genetic	Moderate-to-large genetic influence on the overlap between victimization experiences and delinquency involvement.
Barnes <i>et al.</i>	2012	Add Health	Behavior Genetic	Small-to-moderate genetic influence on gang membership and victimization experiences from adolescence to adulthood.
Barnes <i>et al.</i>	2011	Add Health	Behavior Genetic	Moderate-to-large genetic influence on <i>life-course-persistent</i> (LCP) offending. Moderate genetic influence on abstaining. Small-to-moderate genetic influence on adolescence-limited (AL) offending.
Barnes & Boutwell	2012	Add Health	Behavior Genetic	Moderate genetic influence on delinquency in adolescence and criminality in adulthood. Large genetic influence on stability of criminal behavior over time. Environmental factors accounted for change.
Beaver	2011	Add Health	Behavior Genetic	Small-to-large genetic influences on perceptions of parenting (attachment, involvement, disengagement, and negativity).
Beaver <i>et al.</i>	2008	Add Health	Behavior Genetic	Moderate-to-large genetic influence on measures of self-control across two waves. Genetic influences accounted for large portion of stability in self-control over time.
Beaver <i>et al.</i>	2009(a)	Add Health	Behavior Genetic	Moderate-to-large genetic influences on victimization experiences across two time periods. Genetic factors explained much of the stability in victimization over time.
Beaver <i>et al.</i>	2009(c)	Add Health	Behavior Genetic	Moderate-to-large genetic influences on levels of self-control and delinquent peer affiliation. Few parenting factors operated as nonshared environmental influences on self-control or delinquent peer affiliation.

Beaver <i>et al.</i>	2010(b)	Add Health	Behavior Genetic	Moderate-to-large portions of the covariance between self-control and parenting was due to shared genetic influences. The remaining covariance was due to nonshared environmental factors, suggesting child-driven effects are important.
Beaver <i>et al.</i>	2011(a)	Add Health	Behavior Genetic	Moderate genetic influences on psychopathy score. Genetic risk for psychopathy predicts parental responses to individual.
Beaver <i>et al.</i>	2011(b)	Add Health	Behavior Genetic	Large portion of the variance in delinquent peer association attributed to genetic factors. More than half of the stability in delinquent peer affiliation over time attributed to genetic influences.
Beaver <i>et al.</i>	2011(d)	Add Health	Behavior Genetic	Male adoptees who had a biological father who was criminal scored high on a measure of psychopathy compared to other males.
Boisvert <i>et al.</i>	2012	Add Health	Behavior Genetic	Moderate-to-large genetic influences on self-control and delinquency/criminality individually. Genetic overlap explained much of the correlation between self-control and delinquency/criminality.
Larsson <i>et al.</i>	2008	TEDS	Behavior Genetic	Substantial genetic influence on callous-unemotional traits.
McCartan	2007	NLSY	Behavior Genetic	Substantial genetic influence on antisocial behavior. Nonshared environment (and error) also important.
Rodgers <i>et al.</i>	2001	NLSY	Behavior Genetic	Moderate genetic influence on delinquency. Genetic factors interact with environment.
				Moderate genetic influence on delinquency. Nonshared environment (and error) also important.

(Continued)

Table 5.1 (Continued)

Author(s)	Year	Data	Analysis Type	Primary Finding(s)
Vaske <i>et al.</i>	2012	Add Health	Behavior Genetic	Moderate genetic influence on criminal behavior and violent victimization individually. Small-to-moderate genetic influence on correlation between criminal behavior and violent victimization.
Westerlund <i>et al.</i>	2010	Finland	Behavior Genetic	Moderate genetic influences on sociosexual behavior, sociosexual attitudes, and sexual coercion. Genetic factors common to each measure explained a portion of their correlation.
Wright & Beaver	2005	ECLS-K	Behavior Genetic	After accounting for genetic influences on self-control, parenting effects had weak and inconsistent effects.
Beaver	2008	Add Health	Molecular Genetic	A genetic risk index (including <i>DRD2</i> , <i>DRD4</i> , and <i>DAT1</i>) interacts with childhood exposure to abuse to predict violent delinquency for males.
Beaver <i>et al.</i>	2007	Add Health	Molecular Genetic	Variants of the <i>DRD2</i> gene interact with delinquent peers to predict victimization for White males.
Beaver <i>et al.</i>	2010(a)	Add Health	Molecular Genetic	Variants of the <i>MAOA</i> gene interact with neuropsychological deficits to predict delinquency and self-control for White males.
Beaver <i>et al.</i>	2009(b)	Add Health	Molecular Genetic	Variants of the <i>5HTT</i> gene interact with delinquent peers to predict self-control in adolescence and adulthood.
Beaver <i>et al.</i>	2011(c)	Add Health	Molecular Genetic	Variants of the <i>DRD2</i> gene, the <i>DAT1</i> gene, and the <i>5HTT</i> gene predict victimization experiences (resiliency to victimization).
Beaver <i>et al.</i>	2012	Add Health	Molecular Genetic	Variants of the <i>DRD2</i> gene and the <i>DRD4</i> gene interact with neighborhood disadvantage to predict victimization (<i>DRD4</i>), association with delinquent peers (<i>DRD2</i>), and violent delinquency (<i>DRD2</i> & <i>DRD4</i>) for males.

DeLisi <i>et al.</i>	2009	Add Health	Molecular Genetic	<p> Variants of the <i>DRD2</i> gene interact with criminal father to predict serious delinquency, violent delinquency, and number of police contacts. Variants of the <i>MAOA</i> gene interact with perceived prejudice to predict arrest for males. Variants of the <i>5HTT</i> gene, the <i>DRD4</i> gene, and the <i>MAOA</i> gene, interact with hostile/demoralizing environment to predict aggression and adoption of street code. Variants of the <i>DRD2</i> gene predict victimization among self-reported offenders. Variants of the <i>DAT1</i> gene predict neurocognitive skills and delinquent peers. Variants of the <i>DRD2</i> gene predict neurocognitive skills and maternal withdrawal. Variants of the <i>DRD4</i> gene and the <i>DAT1</i> gene interact with maternal negativity to predict levels of self-control. Variants of the <i>DAT1</i> gene predict a direct measure of peer delinquency (i.e., social network measure) for White males from high-risk families. </p>
Schwartz & Beaver	2011	Add Health	Molecular Genetic	
Simons <i>et al.</i>	2012	FACHS	Molecular Genetic	
Vaske <i>et al.</i>	2011a	Add Health	Molecular Genetic	
Vaughn <i>et al.</i>	2009	Add Health	Molecular Genetic	
Wright <i>et al.</i>	2012	Add Health	Molecular Genetic	
Yun <i>et al.</i>	2011	Add Health	Molecular Genetic	

In general, four key findings emerged from the extant behavior genetic research in criminology. First, measures of crime, criminality, and delinquency evince moderate-to-large genetic influences (e.g., Rodgers *et al.*, 2001). In other words, genetic factors appear to have a significant influence on variance in delinquency, criminal behavior, and measures of self-control. The environment also emerged as a salient predictor of variance. It is important to point out, however, that nonshared environmental influences were the predominant environmental factor. The second key finding to emerge was that a small-to-moderate portion of the variance in victimization experiences is due to genetic influences (e.g., Vaske *et al.*, 2012). The third key finding from behavior genetic research is that much of the overlap between key concepts in criminology (e.g., victim-offender overlap, self-control and delinquency overlap, psychopathy and negative parenting, etc.) is the result of genetic factors operating on both outcomes (e.g., Barnes & Beaver, 2012; Boisvert *et al.*, 2012). Finally, the fourth key finding to emerge from the behavior genetic research is that, after including controls for genetic influences, parenting measures tend to exhibit a null or weakened effect on levels of self-control and other similar constructs (Wright & Beaver, 2005). It is worth pointing out that all but one study (Beaver *et al.*, 2011d) used the twin method (or a variant of the twin study). Beaver and colleagues (2011d) analyzed a sample of adoptees and reported a correlation between biological father's arrest record and the child's score on a measure of psychopathy in adulthood.

Molecular genetic findings

The final set of findings presented in Table 5.1 summarizes the biosocial criminological literature that has utilized a molecular genetic analysis strategy. A total of 13 studies were identified and the key findings from each are presented in the table. To summarize briefly, each of the studies identified a correlation between a particular genetic polymorphism and some form of antisocial behavior or a correlate of offending, such as self-control. All but one study utilized molecular genetic data available in the Add Health data. The lone exception was Simons and colleagues who drew on data from the Family and Community Health Study (FACHS). A total of five genes were analyzed across the 12 studies. The genes analyzed were three dopamine receptor or transporter genes (*DRD2*, *DRD4*, and *DAT1*), a serotonin transporter gene (*5HTT*), and the monoamine oxidase a gene (*MAOA*). Each study provides a unique outlook on the relationship between certain genetic polymorphisms and antisocial behavior. Two points, however, offer a concise summary of the available literature. First, though these five genes make up only a fraction of the human genome, each has been shown to correlate with antisocial outcomes, indicating the importance of genotype in the etiology of human antisocial behavior. Second, many of the studies reviewed (e.g., Simons *et al.*, 2012; Wright *et al.*, 2012) revealed the complex nature of human behavior by indicating that genetic effects alone were not enough to predict antisocial outcomes. Instead, several studies reported an

interaction between genotype and environmental factors. In other words, *both* genetic risk *and* environmental risk were necessary to understand the etiology of antisocial behavior (e.g., Beaver, 2008).

Discussion

Biosocial criminology is an emerging paradigm that has much to offer to the criminological discipline (Wright & Boisvert, 2009). Some of the most exciting offerings brought by biosocial criminology are the opportunities to investigate new ideas, incorporate new research methodologies, and increase theoretical potency (Wright & Boisvert, 2009). The goal of the current study was to summarize the recent biosocial criminological literature. In doing so, we suggest that contemporary biosocial criminology includes five domains of research: evolutionary criminology, biological criminology, behavior genetics, molecular genetics, and neurocriminology. Research bearing on the first four domains was included in the review. We did not assess the neurocriminological research because these studies have almost exclusively been published in journals outside of the criminological discipline. This is not to suggest that neurocriminology is inferior to the other domains, that it is less developed, or that it is in anyway less important. To be sure, some of the most fascinating findings of the 21st century have come out of neuroscience laboratories (Moffitt *et al.*, 2011). Unfortunately, the parameters of our literature search did not capture any of these studies.

Although biosocial criminology has begun to “come of age” over the past decade, it was somewhat surprising that so few studies were captured by our literature search. Indeed, barely more than 300 articles were captured by the initial search criteria. Once a manual inclusion process was carried out, this number was whittled down to less than 50. Though this is an improvement over previous decades, where the modal value for biosocial criminology research likely hovered in the single digits, 41 studies is far fewer than the number of studies testing mainstream criminological theories (i.e., the majority of studies captured by our initial search). It should be noted that the constraints placed on our literature search undoubtedly led to certain papers being overlooked (e.g., Cauffman *et al.*, 2005). This limitation, however, is unlikely to have led to the omission of a large body of research. Because we remain optimistic about the future of biosocial criminological research, we take this opportunity to highlight the need for much more attention and research into the different domains of the paradigm.

As for current efforts, five broad findings (with a few sub-points) emerged from the systematic review:

- 1 Genetic influences are important to consider when analyzing the etiology of antisocial behavior.
 - 1.a Behavior genetic research has shown that a moderate-to-large amount of the variance in antisocial behaviors (and its antecedents) is attributable to genetic factors.

- 1.b Molecular genetics research has begun to identify specific genetic polymorphisms linked to antisocial behavior (and its antecedents).
- 2 Though biosocial criminology has repeatedly shown genetic factors to be important in the etiology of antisocial behavior, these research studies have also highlighted the importance of the environment.
- 2.a Behavior genetic research has shown the environment to explain a substantial portion of the variance in antisocial behavior. But, it is important to distinguish between shared and nonshared environments.
- 2.a.i Shared environments tend to have a negligible impact on variance in antisocial behaviors.
- 2.a.ii Nonshared environments appear to explain the largest portion of environmental variance in antisocial behaviors.
- 3 Biosocial research reveals the synergistic relationship between genes and environments. It is not nature vs. nurture, it is both. Genes and environments *interact* to create behavioral outcomes.
- 4 The brain mediates the genetic effect (or much of it) identified by behavior genetics and molecular genetics research.
- 4.a In other words, criminologists must begin to familiarize themselves with biological and neuroscience research. The absence of neurocriminological research in criminology journals is telling and must be addressed by today's scholars.
- 5 Evolutionary forces have shaped human development over eons. Evolutionary criminology recognizes this point and proposes answers to some of the "hard questions" such as why males are over-involved in violence.
- 5.a Evolution can also raise new questions that have, heretofore, been ignored/unconsidered such as "why do siblicide perpetrators use violence when killing a sibling-in-law more often than when killing a full sibling?" (Michalski *et al.*, 2007).

In light of these observations, we conclude by drawing attention to two final points. The first point concerns the current state of criminological theory. Given the momentum of the biosocial paradigm, it may seem natural for scholars to ask whether there is a "biosocial theory" or whether we need a biosocial theory. As noted in this review, several scholars have begun to integrate biosocial tenets into extant criminological theories. Agnew's (1992) general strain theory appears to be one of the most popular for this type of integration (Schroeder *et al.*, 2011; Stogner & Gibson, 2010; Walsh, 2000). Other theories ripe for integration or adoption by the biosocial paradigm are Moffitt's (1993) developmental taxonomy (Barnes *et al.*, 2011), Gottfredson & Hirschi's (1990) self-control theory (Wright & Beaver, 2005), and Akers' social learning theory (Beaver *et al.*, 2011b). Given the wealth of criminological theories available to researchers, it is our position that the biosocial paradigm does not need a "new" theory. Instead, the biosocial paradigm is likely to continue gaining momentum by integrating new insights and ideas into existing theories.

The second point that must be considered by criminologists and biosocial criminologists alike is whether biosocial criminology has any insight into treatment or

policy. Some scholars have argued very persuasively that biosocial criminology can and should inform public policy and intervention efforts (Maletzky & Field, 2003; Solomon & Heide, 2005; Vaske *et al.*, 2011). Nonetheless, criminologists remain skeptical about the value of adding a biosocial component to treatment, whether it will be harmful, and whether we have enough information to implement such a policy (Barnes, 2014). While we agree that there is still much to be learned from biosocial research before any holistic biosocial policy/intervention would be possible, the current knowledge base is very clear that the integration of biosocial criminological findings into policy discussions and intervention strategies is possible, it is promising, and it is no more dangerous than standard criminological policy/intervention.

In the years to come, scholars of crime will be forced to contemplate a handful of related, and very important, questions. Specifically, will we join the ranks of scientists who dispassionately examine evidence, formulate hypotheses free of ideological constraints, and test scientific questions without fear of what the results might say? We have no answer for this question now, only the hope that moving forward, all questions – regardless of their political correctness (or lack thereof) – will be fully on the table.

Notes

- 1 To say that females invest more heavily does not negate the role of fathers in a modern society. Certainly, human fathers often invest quite heavily in their children, both emotionally and via the contribution of resources (i.e., protection, food, shelter, etc.). Even so, male investment cannot fully approach that of female investment for the simple fact that females gestate the fetus for nine months, all the while expending calories to the developing embryo. Moreover, females are limited in the number of eggs they can produce in a lifetime, whereas male production of sperm remains considerable for long stretches of the life-course.
- 2 Again, we recognize that there is a host of evolutionary psychological research bearing on the subject of aggression and violence. For the sake of brevity in this review, we opted to focus on those studies conducted by scholars with a criminological focus.

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